

SCORE Search Results Details for Application 10529592 and Search Result 20090427_122917_us-10-529-592a-1.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 10529592 and Search Result 20090427_122917_us-10-529-592a-1.rst.

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GenCore version 6.3

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OM nucleic - nucleic search, using sw model

Run on: April 28, 2009, 04:16:35 ; Search time 1875 Seconds
(without alignments)
45457.283 Million cell updates/sec

Title: US-10-529-592A-1
Perfect score: 881
Sequence: 1 gggccatgacccccgctgct.....aaataaagatcctctgtaac 881

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 83780570 seqs, 48372533981 residues

Total number of hits satisfying chosen parameters: 167561140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*

9: gb_est9:*
 10: gb_est10:*
 11: gb_est11:*
 12: gb_est12:*
 13: gb_est13:*
 14: gb_est14:*
 15: gb_est15:*
 16: gb_est16:*
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 18: gb_est18:*
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 20: gb_gss2:*
 21: gb_gss3:*
 22: gb_gss4:*
 23: gb_gss5:*
 24: gb_gss6:*
 25: gb_gss7:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	710.6	80.7	979	5	BQ672221	BQ672221 AGENCOURT
2	703	79.8	916	5	BU527159	BU527159 AGENCOURT
3	685.6	77.8	735	4	BI914593	BI914593 603179545
4	650.4	73.8	889	5	BQ671560	BQ671560 AGENCOURT
5	563	63.9	586	3	BE875115	BE875115 601485988
c 6	549	62.3	687	4	BM977476	BM977476 UI-CF-EN1
c 7	547.4	62.1	677	4	BQ045152	BQ045152 UI-CF-EN1
8	545.6	61.9	840	4	BI546970	BI546970 603190185
9	545.4	61.9	838	7	CF993841	CF993841 AGENCOURT
c 10	543.8	61.7	600	1	AA760709	AA760709 nz13c11.s
c 11	539.8	61.3	573	4	BQ025351	BQ025351 UI-1-BB1p
c 12	539.8	61.3	581	4	BQ025360	BQ025360 UI-1-BB1p
13	536.4	60.9	591	4	BM711587	BM711587 UI-E-CL1-
c 14	536	60.8	539	1	AI973037	AI973037 wr46g08.x
15	530.2	60.2	843	7	CB993691	CB993691 AGENCOURT
16	510.2	57.9	577	5	BQ425608	BQ425608 AGENCOURT
c 17	501.4	56.9	541	4	BQ025279	BQ025279 UI-1-BB1p
18	501.2	56.9	542	4	BM688675	BM688675 UI-E-CQ1-
c 19	491	55.7	495	2	AW072412	AW072412 xa07f07.x
c 20	486.4	55.2	491	1	AI969836	AI969836 wq75f01.x
21	474	53.8	474	4	BM725994	BM725994 UI-E-EJ0-
22	472.4	53.6	788	7	CD101714	CD101714 AGENCOURT

	23	460.6	52.3	593	18	W56389	W56389	zc57b01.r1
c	24	453	51.4	456	1	AI824062	AI824062	wj35f10.x
c	25	452.4	51.4	469	4	BM681000	BM681000	UI-E-EJ0-
c	26	447.4	50.8	460	1	AI201581	AI201581	qc02g09.x
	27	438.4	49.8	443	8	CN366258	CN366258	170006008
c	28	434.8	49.4	456	5	BU727045	BU727045	UI-E-CQ1-
	29	433	49.1	447	7	CD674248	CD674248	fs08d06.y
c	30	417.6	47.4	439	2	AW779356	AW779356	hn80b03.x
	31	417	47.3	626	4	BM688212	BM688212	UI-E-CL0-
	32	416.2	47.2	803	7	CB998149	CB998149	AGENCOURT
c	33	404.8	45.9	412	1	AI042370	AI042370	ox62b07.x
c	34	404	45.9	429	1	AA827147	AA827147	ob53c05.s
	35	397	45.1	398	5	BX096382	BX096382	BX096382
	36	383.6	43.5	413	1	AA490346	AA490346	aa44a05.r
c	37	380	43.1	381	1	AI221443	AI221443	qg75c09.x
	38	372.8	42.3	616	3	BG285710	BG285710	602380756
	39	367	41.7	574	18	W37398	W37398	zc11a10.r1
c	40	360	40.9	365	2	AW419070	AW419070	ha17c11.x
c	41	357.4	40.6	361	2	AW439942	AW439942	hal1e11.x
c	42	356.4	40.5	384	5	BU726946	BU726946	UI-E-CL0-
c	43	351.4	39.9	366	1	AI216467	AI216467	qh07h08.x
c	44	351.2	39.9	386	18	N98734	N98734	zb87f07.s1
	45	338.4	38.4	1094	4	BM925906	BM925906	AGENCOURT

ALIGNMENTS

RESULT 1

BQ672221

LOCUS BQ672221 979 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8303632 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6274816
 5', mRNA sequence.

ACCESSION BQ672221

VERSION BQ672221.1 GI:21783055

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 979)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM2456 row: p column: 17
 High quality sequence stop: 550.

FEATURES
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 1. .979
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6274816"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 80.7%; Score 710.6; DB 5; Length 979;
 Best Local Similarity 97.3%; Pred. No. 1.7e-163;
 Matches 786; Conservative 0; Mismatches 15; Indels 7; Gaps 6;

Qy	1	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGGAGCCCGAC	60
Db	23	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGGAGCCCGAC	82
Qy	61	CGCCGCCGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCTCGGGCGCGGCTCCGC	120
Db	83	CGCCGCCGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCTCGGGCGCGGCTCCGC	142
Qy	121	AGTGAGCCCAACAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	143	AGTGAGCCCAACAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	202
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCG	240
Db	203	TGCCTGAAAGGCTTTCAAATGTGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCG	262
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCAG	300
Db	263	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCAG	322

Qy 301 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 360
 |||
 Db 323 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 382

Qy 361 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG 420
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 Db 383 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG 442

Qy 421 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
 |||
 Db 443 CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 502

Qy 481 CTGAATACCTTGGATGGGAACCTGAGCGAA-CCCGGGCCTCCGCTCAGAGAGACGTGGCAG 539
 |||
 Db 503 CTGAATACCTTGGATGGGAACCTGAGCGAACC CGGGCCTCCGCTCAGAGAGACGTGGCAG 562

Qy 540 GACCAGCGAGGAATCCAGCCTGTCCA-CTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAG 598
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 Db 563 GACCAGCGAGGAATCCAGCCTGTCCACCTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAG 622

Qy 599 TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC 658
 |||
 Db 623 TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGNTGAAAGGGAGCGC 682

Qy 659 CATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGCTCT-CTTCTGGACAAACACACCC-TC 716
 |||
 Db 683 CATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTCTTCTGGACAAACACACCTTC 742

Qy 717 CCAGCCCCCAGGGCTGTGCAAAACACATG-CCCCTGCCATAAGCACCAACAAGAAC--TTC 773
 |||
 Db 743 CCAGCCCCCAGGGCTGTGCAAAACACATGCCCGGCCATAAGCCCCACAAAACCTTCT 802

Qy 774 TTGCAGGTGGAGTGGCTGTTTTTTTATAA 801
 |||
 Db 803 TGGCCGGGGGAAGGGCTTTTTTTTTTAA 830

RESULT 2

BU527159

LOCUS BU527159 916 bp mRNA linear EST 13-SEP-2002

DEFINITION AGENCOURT_10154878 NIH_MGC_101 Homo sapiens cDNA clone
 IMAGE:6536921 5', mRNA sequence.

ACCESSION BU527159

VERSION BU527159.1 GI:22837600

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2699 row: a column: 17
 High quality sequence stop: 653.

FEATURES
 source Location/Qualifiers
 1. .916
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6536921"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_101"
 /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 79.8%; Score 703; DB 5; Length 916;
 Best Local Similarity 96.9%; Pred. No. 1.2e-161;
 Matches 749; Conservative 0; Mismatches 20; Indels 4; Gaps 3;

Qy	1	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGCCGAGCCCGAC	60
Db	3	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCGCCGAGCCCGAC	62
Qy	61	CGCCGCCGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGGGCTCCGC	120
Db	63	CGCCGCCGCCACCAACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGGGCTCCGC	122
Qy	121	AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180

```

|||||
Db      123 AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC 182
Qy      181 TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 240
|||||
Db      183 TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCCACGACGAGGCCCCC 242
Qy      241 GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCAGCCCCCACCACCCACG 300
|||||
Db      243 GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCAGCCCCCACCACCCACG 302
Qy      301 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 360
|||||
Db      303 GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC 362
Qy      361 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG 420
|||||
Db      363 CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG 422
Qy      421 CTCCTGCTCCAGCGGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 480
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Db      423 CTCCTGCTCCAGCGGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG 482
Qy      481 CTGAATACCCTGGATGGGAACCTGAGCGAACCCTGGGCTCCGCTCAGAGAGACGTGGCAGG 540
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Db      483 CTGAATACCCTGGATGGGAACCTGAGCGAACCCTGGGCTCCGCTCAGAGAGACGTGGCAGG 542
Qy      541 ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTG 600
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Db      543 ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTG 602
Qy      601 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 660
|||||
Db      603 GACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCA 662
Qy      661 TGGTCCTGGC--TGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCT-CC 717
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Db      663 TGGTCCTGGCCTGGTGGGGTCCCAGGGAAGAGGCTCTCTTCTGGACAAACACACCCTCCC 722
Qy      718 CAGCCCCCAGGGCTGTG-CAAACACATGCCCTGCCATAAGCACCAACAAGAA 769
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Db      723 CAGCCCCCAGGGCTGTGCCAAACCATGCCCCCTGCCAATAAGGCACCAACAA 775

```

RESULT 3

BI914593

LOCUS BI914593 735 bp mRNA linear EST 16-OCT-2001

DEFINITION 603179545F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243626 5', mRNA sequence.

ACCESSION BI914593
 VERSION BI914593.1 GI:16178714
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 735)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11614 row: j column: 11
 High quality sequence stop: 723.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5243626"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."
 ORIGIN
 Query Match 77.8%; Score 685.6; DB 4; Length 735;
 Best Local Similarity 96.6%; Pred. No. 2.3e-157;
 Matches 730; Conservative 0; Mismatches 4; Indels 22; Gaps 2;
 Qy 119 GCAGTGAGCCACCAAGAAGGAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGT 178
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Db	1	GCAGTGAGCCCAACGAAGGAGCGGCCTGCAGAGGTGCCGACATGGGGCTTAAGATGT	60
Qy	179	CCTGCCTGAAAGGCTTTCAAATGTGTGTGCAGCAGCAGCAGCAGCCACGACGAGGCCC	238
Db	61	CCTGCCTGAAA-----TGCAGCAGCAGCAGCCACGACGAGGCCC	99
Qy	239	CCGTCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCCECA	298
Db	100	CCGTCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCCECA	159
Qy	299	CGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGT	358
Db	160	CGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGT	219
Qy	359	GCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCT	418
Db	220	GCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCT	279
Qy	419	GGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTG	478
Db	280	GGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTG	339
Qy	479	TGCTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCCTCCGCTCAGAGAGACGTGGCA	538
Db	340	TGCTGAATACCCTGGATGGGAACTGAGCGAACC CGGCCCTCCGCTCAGAGAGACGTGGCA	399
Qy	539	GGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCAGGCCCGCTGAG	598
Db	400	GGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCAGGCCCGCTGAG	459
Qy	599	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC	658
Db	460	TGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGC	519
Qy	659	CATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCC	718
Db	520	CATGGTCTGGCTGTTGGGGTCCCAGGCAGAGGCTCTCTTCTGGACAAACACACCCTCCC	579
Qy	719	AG-CCCCAGGGCTGTGCAAAACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGC	777
Db	580	AGCCCCCAGGGCTGTGCAAAACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGC	639
Qy	778	AGGTGGAGTGGCTGTTTTTATAAGTTGTTTACAGATACGGAACAGTCCAAAATGGGA	837
Db	640	AGGTGGAGTGGCTGTATTTTATAAGTTGTTTACAGATACGGAACAGTCCAAAATGGGA	699
Qy	838	TTTATAATTCTTTTTTGCATTATAAATAAAGATCC	873
Db	700	TTTATAATTCTTTTTTGCATTATAAATAAAGATCC	735

RESULT 4
 BQ671560
 LOCUS BQ671560 889 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8171941 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6277428
 5', mRNA sequence.
 ACCESSION BQ671560
 VERSION BQ671560.1 GI:21782394
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 889)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2463 row: m column: 13
 High quality sequence stop: 549.
 FEATURES
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 1. .889
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6277428"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.8%; Score 650.4; DB 5; Length 889;
 Best Local Similarity 93.1%; Pred. No. 1.1e-148;
 Matches 715; Conservative 0; Mismatches 46; Indels 7; Gaps 3;

Qy	1	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	23	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	82
Qy	61	CGCGCGCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	120
Db	83	CGCGCGCGCCACCACCACCAGCGCCCGGGCGGGCCTCGCGCGCCTCGGGCGCGGCTCCGC	142
Qy	121	AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	143	AGTGAGCCACCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	202
Qy	181	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	240
Db	203	TGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	262
Qy	241	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG	300
Db	263	GTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATCACGCCCCCACCACCCACG	322
Qy	301	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	360
Db	323	GGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGC	382
Qy	361	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG	420
Db	383	CCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGG	442
Qy	421	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	480
Db	443	CTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTG	502
Qy	481	CTGAATACCCTGGATGGGAACAGAGCAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG	540
Db	503	CTGAATACCCTGGATGGGAACAGAGCAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGG	562
Qy	541	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGG-CCCCGCTGAGT	599
Db	563	ACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGGCCCCCGCTGAGG	622
Qy	600	GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC	659
Db	623	GGACCGGACCTCTGACACCTCCCGGTTCTTGCTGACTCCGGCCTGGGGAAAGGGAACCGC	682
Qy	660	ATGGTCC--TGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGACAAACACACCTCC	717

```

      ||||| | | ||| ||||| || | | | ||| | | | |||
Db      683 TTGGTCCCTGGCTGTTGGGGGGCCAGGGAAGGGTCGTCCTTCGGAGCAAACGAACCTTT 742

Qy      718 CA----GCCCCCAGGGCTGTGCAACACATGCCCTGCCATAAGCACC 761
      | |||| | | ||| | ||| | ||| | |||
Db      743 GAAAGCCCCCCGGGCATGGACAAAACAAGCCCCGGTCCTATGGACC 790

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RESULT 5

BE875115

LOCUS BE875115 586 bp mRNA linear EST 20-OCT-2000

DEFINITION 601485988F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888621 5', mRNA sequence.

ACCESSION BE875115

VERSION BE875115.1 GI:10323891

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 586)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9668 row: o column: 22

High quality sequence stop: 586.

FEATURES Location/Qualifiers

source

1..586

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3888621"

/tissue_type="large cell carcinoma, undifferentiated"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_69"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 63.9%; Score 563; DB 3; Length 586;
 Best Local Similarity 99.0%; Pred. No. 3.4e-127;
 Matches 577; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      300 GGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTG 359
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Db      1   GGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTG 60

Qy      360 CCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTG 419
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Db      61   CCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTG 120

Qy      420 GCTCTGTCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGT 479
          |||
Db      121  GCTCTGTCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGT 180

Qy      480 GCTGAATACCCTGGATGGGAAGTGTAGCGAACC CGGCTCCGCTCAGAGAGACGTGGCAG 539
          |||
Db      181  GCTGAATACCCTGGATGGGAAGTGTAGCGAACC CGGCTCCGCTCAGAGAGACGTGGCAG 240

Qy      540 GACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCAGGCCCGCTGAGT 599
          |||
Db      241  GACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCCAGGCCCGCTGAGT 300

Qy      600 GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC 659
          |||
Db      301  GGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCC 360

Qy      660 ATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCA 719
          |||
Db      361  ATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCTCCCA 420

Qy      720 GCCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAG 779
          |||
Db      421  GCCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAG 480

Qy      780 GTGGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGAAACAGTCCAAAATGGGATT 839
          |||
Db      481  GTGGAGTGGCTGTTTTTTATAAGTCGTTTTACAGATACGAAACAGTCCAAAATGGGATT 540

Qy      840 TATAATTTCTTTTTTGCAATTA-TAAATAAAGATCCTCTGTAAC 881
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Db      541  TATAATTTCTTTTTTGCAATTA-TAAATAAAGATCCTCTGTAAC 583
  
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RESULT 6
 BM977476/c

LOCUS BM977476 687 bp mRNA linear EST 21-FEB-2003

DEFINITION UI-CF-EN1-ae-b-14-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-ae-b-14-0-UI 3', mRNA sequence.

ACCESSION BM977476

VERSION BM977476.1 GI:19595931

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 687)

AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source Location/Qualifiers
1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-ae-b-14-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h TAG_LIB=UI-CF-EN1 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 62.3%; Score 549; DB 4; Length 687;
 Best Local Similarity 100.0%; Pred. No. 9.6e-124;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
Db	575	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	516
Qy	393	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	452
Db	515	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	456
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	512
Db	455	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	396
Qy	513	GGGCTCCGCTCAGAGAGACGTGGCAGGACGAGCAGGAATCCAGCCTGTCCACTTCCAG	572
Db	395	GGGCTCCGCTCAGAGAGACGTGGCAGGACGAGCAGGAATCCAGCCTGTCCACTTCCAG	336
Qy	573	AACAGTGTTCAGGAGGCGGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	632
Db	335	AACAGTGTTCAGGAGGCGGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGCT	276
Qy	633	GACTCCGGCTGGTGAAAGGAGCGCCATGGTCCTGGCTGTTGGGGTCCAGGGAGAGGC	692
Db	275	GACTCCGGCTGGTGAAAGGAGCGCCATGGTCCTGGCTGTTGGGGTCCAGGGAGAGGC	216
Qy	693	TCTCTTCTGGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACACATGCCCTGCC	752
Db	215	TCTCTTCTGGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACACATGCCCTGCC	156
Qy	753	ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACA	812

Db 155 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACA 96

Qy 813 GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAAATAAGATC 872
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Db 95 GATACGGAAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAAATAAGATC 36

Qy 873 CTCTGTAAC 881
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Db 35 CTCTGTAAC 27

RESULT 7
 BQ045152/c

LOCUS BQ045152 677 bp mRNA linear EST 21-FEB-2003

DEFINITION UI-CF-EN1-acl-o-16-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acl-o-16-0-UI 3', mRNA sequence.

ACCESSION BQ045152

VERSION BQ045152.1 GI:19796231

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 677)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES Location/Qualifiers

source 1..677

/organism="Homo sapiens"


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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-ael-o-16-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT. TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h TAG_LIB=UI-CF-EN1 TAG_SEQ=CTGCTCAGGT"

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ORIGIN

Query Match 62.1%; Score 547.4; DB 4; Length 677;
 Best Local Similarity 99.8%; Pred. No. 2.4e-123;
 Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	333	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	392
Db	564	AGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCCTG	505
Qy	393	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	452
Db	504	AGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCC	445
Qy	453	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	512
Db	444	GGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTGAAGCAACCC	385
Qy	513	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	572
Db	384	GGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAG	325
Qy	573	AACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGACCTCTGACACCTCCAGGTTCTTGCT	632

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|||||
Db      324 AACAGTGTTCCTCCAGGCCCGCTGAGTGACCGGACCTCTGACACCTCCAGGTTCTTGCT 265

Qy      633 GACTCCGGCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 692
|||||
Db      264 GACTCCGGCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGC 205

Qy      693 TCTCTTCTGGACAAACACACCCCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCC 752
|||||
Db      204 TCTCTTTTGGACAAACACACCCCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCC 145

Qy      753 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 812
|||||
Db      144 ATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGTTTTACA 85

Qy      813 GATACGGAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAATAAGATC 872
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Db      84  GATACGGAACAGTCCAAAATGGGATTATAATTTCTTTTTTGCAATTATAAATAAGATC 25

Qy      873 CTCTGTAAC 881
|||||
Db      24  CTCTGTAAC 16

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RESULT 8

BI546970

LOCUS BI546970 840 bp mRNA linear EST 05-SEP-2001
 DEFINITION 603190185F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261660 5', mRNA sequence.

ACCESSION BI546970

VERSION BI546970.1 GI:15434282

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 840)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11659 row: i column: 21
 High quality sequence stop: 737.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5261660"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_95"
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.9%; Score 545.6; DB 4; Length 840;
 Best Local Similarity 89.1%; Pred. No. 6.8e-123;
 Matches 709; Conservative 0; Mismatches 34; Indels 53; Gaps 9;

Qy	1	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	60
Db	49	GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTCGCCGCGGCCCCCGAGCCCGAC	108
Qy	61	CGCGCGCGCCACCACCAGCGCCGGGCGGGCCTCGCGCGCCTCGGGCGGGCTCCGC	120
Db	109	CGCGCGCGCCACCACCAGCGCCGGGCGGGCCTCGCGCGCCTCGGGCGGGCTCCGC	168
Qy	121	AGTGAGCCCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	180
Db	169	AGTGAGCCCAAGAAGGAAGCGGCTGCAGAGGTGCCGACATGGGGCTTAAGATGTCC	228
Qy	181	TGCCTGAAAG-----GCTTTCAA	198
Db	229	TGCCTGAAAGACGCCGGTTTTTCATCTGTGATGCGGGACAGCTGCGCTCCTTGCTGCGAG	288
Qy	199	ATGTGTGTTCAGCAGCAGCAGCCACGACGAGGCCCCGTCCTGAACGACAAGCAC	258
Db	289	GCGTCAGGACCCAGCAGCAGCAGCCACGACGAGGCCCCGTCCTGAACGACAAGCAC	348

Qy	259	CTGGACGTGCCCCGACATCATCATCACGCCCCCACCACGGGCATGATGCTGCCGAGG	318
Db	349	CTGGACGTGCCCCGACATCATCATCACGCCCCCA-CCCCACGGGCATGATGCTGCCGAGG	407
Qy	319	GACTTGGGGAGCAGACTCTGGCTGG-ATGAGACAGGGTCGTGCCAGATGATGGAGAAAT	377
Db	408	GACTTGGGGAGCAGACTCTGGCTGGCATGAGACAGGGTCGTGCCAGATGATGGAGAAAT	467
Qy	378	CGACCCAGAAGCCTGAGGAGGTGCTCTGGGTTTGCTGGCTGGCTCCTGCTCCAGCGGCC	437
Db	468	CGACCCAGAAGCCTGAGGAGGTGCTCTGGGTTTGCTGGCTGGCTCCTGCTCCAGCGGCC	527
Qy	438	CGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGG	497
Db	528	CGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGG	587
Qy	498	GAAC-TGAGCGAACC CGGCCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCA	556
Db	588	GAACCTGAGCGAACC CGGCCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCA	647
Qy	557	GCCTGTCCACTTCCAGAA-CAGTGTTTCCAGGCCCCGCTG-AGTGGACCGGACCTC-TG	613
Db	648	GCCTGTCCACTTCCAGAACCACTGTTTACAGGCCCCGCTGAAGTGGACCGGACCTCTTG	707
Qy	614	ACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTTGCTGT	673
Db	708	ACACCTCCAGGTTCTTGCTGACTCCGGCCTGTTGAAAGGGAACGCCATGGTCTTGCTGT	767
Qy	674	TGG--GGTCCAGGGAGAGGCTCTCTTCTGGACAAACACACCCCTCCAGCCCCAGGGCT	731
Db	768	TGGGAGTCCCAAGGAAGAGGCTCTCTTCTGGACAAACACCTCCAAA--CCCAAGGCT	824
Qy	732	GTGCAACACATGCC	747
Db	825	GTGCCAACACATGCC	840

RESULT 9

CF993841

LOCUS CF993841 838 bp mRNA linear EST 25-NOV-2003

DEFINITION AGENCOURT_15622657 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30705878 5', mRNA sequence.

ACCESSION CF993841

VERSION CF993841.1 GI:38509901

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

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FEATURES
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                /db_xref="taxon:9606"
                /clone="IMAGE:30705878"
                /tissue_type="Human Placenta"
                /lab_host="DH10B TonA"
                /clone_lib="NIH_MGC_147"
                /note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

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Query Match 61.9%; Score 545.4; DB 7; Length 838;
Best Local Similarity 98.9%; Pred. No. 7.6e-123;
Matches 549; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 327 GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA 386
| | | | | ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 16 GCGTAGAACCAAGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA 75

Qy 387 AGCCTGAGGAGGTGTCTGGGTTTGCTGGCTGGCTCCTGCTCCAGCGGCCCCGGCTTCAG 446

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Db      76 AGCCTGAGGAGGTGCTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGCTTCAG 135

Qy      447 GTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTACG 506
|||||
Db      136 GTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAAGTACG 195

Qy      507 GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC 566
|||||
Db      196 GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC 255

Qy      567 TTCCAGAACAGTGTTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT 626
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Db      256 TTCCAGAACAGTGTTTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT 315

Qy      627 CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGG 686
|||||
Db      316 CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGG 375

Qy      687 AGAGGCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAAACACATGCC 746
|||||
Db      376 AGAGGCTCTCTTCTGGACAAACACACCTCCAGCCCCCAGGGCTGTGCAAAACACATGCC 435

Qy      747 CCTGCCATAAGCACCAACAAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTATAAGTTGT 806
|||||
Db      436 CCTGCCATAAGCACCAACAAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTATAAGTTGT 495

Qy      807 TTTACAGATACGGAACAGTCCAAAATGGGATTTATAATTTCTTTTTGCATTATAAATA 866
|||||
Db      496 TTTACAGATACGGAACAGTCCAAAATGGGATTTATAATTTCTTTTTGCATTATAAATA 555

Qy      867 AAGATCCTCTGTAAC 881
|||||
Db      556 AAGATCCTCTGTAAC 570

```

RESULT 10

AA760709/c

LOCUS AA760709 600 bp mRNA linear EST 07-FEB-1998

DEFINITION nt13c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287668 3', mRNA sequence.

ACCESSION AA760709

VERSION AA760709.1 GI:2809639

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

http://es.ScoreAccessWeb/GetItem.action?AppId=105295...7 122917 us-10-529-592a-1.rst&ItemType=4&startByte=0 (23 of 35)5/19/2009 9:51:32 AM

Qy	358	TGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGC	417
Db	541	TGCCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGC	482
Qy	418	TGGCTCCTGCTCCAGCGGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGT	477
Db	481	TGGCTCCTGCTCCAGCGGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCTGCCTGGAGCAGGT	422
Qy	478	GTGCTGAATACCTTGGATGGGAAGTGAAGCAACCCGGGCTCCGCTCAGAGAGACGTGGC	537
Db	421	GTGCTGAATACCTTGGATGGGAAGTGAAGCAACCCGGGCTCCGCTCAGAGAGACGTGGC	362
Qy	538	AGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCAGGCCCCCGCTGA	597
Db	361	AGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCAGGCCCCCGCTGA	302
Qy	598	GTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCG	657
Db	301	GTGGACCGGACCTCTGACACCTCCAGGTTCTTGCTGACTCCGGCCTGGTGAAAGGGAGCG	242
Qy	658	CCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCTCC	717
Db	241	CCATGGTCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCTNN	182
Qy	718	CAGCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGC	777
Db	181	C-CCCCCAGGGCTGTGCAAAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGC	123
Qy	778	A-GGTGGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAACAGTCCAAAATGGG	836
Db	122	AGGGTGGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAACAGTCCAAAATGGG	63
Qy	837	ATTTATAATTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	881
Db	62	ATTTATAATTCTTTTTTGCATTATAAATAAAGATCCTCTGTAAC	18

RESULT 11
BQ025351/c

LOCUS	BQ025351	573 bp	mRNA	linear	EST 27-MAR-2002
DEFINITION	UI-1-BB1p-aud-e-02-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone UI-1-BB1p-aud-e-02-0-UI 3', mRNA sequence.				
ACCESSION	BQ025351				
VERSION	BQ025351.1 GI:19760630				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 573)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. 573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-aud-e-02-0-UI"
/tissue_type="Placenta"
/dev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_P16"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_P16 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG_TISSUE=placenta human full term
TAG_LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN

Query Match 61.3%; Score 539.8; DB 4; Length 573;
Best Local Similarity 99.5%; Pred. No. 1.7e-121;
Matches 552; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	327	GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGA	386
Db	569	GAGGACAGTCTGGCTGGATGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGA	510
Qy	387	AGCCTGAGGAGGTGTCTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	446
Db	509	AGCCTGAGGAGGTGTCTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	450
Qy	447	GTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGC	506
Db	449	TTGTCCGGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGC	390
Qy	507	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	566
Db	389	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	330
Qy	567	TTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	626
Db	329	TTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	270
Qy	627	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTGGGGTCCCAGGG	686
Db	269	CTTGCTGACTCCGGCCTGGTGAAAGGGAGCGCCATGGTCTGGCTGTGGGGTCCCAGGG	210
Qy	687	AGAGGCTCTCTTCTTGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACACATGCC	746
Db	209	AGAGGCTCTCTTCTTGACAAACACACCTCCAGCCCCAGGGCTGTGCAAAACACATGCC	150
Qy	747	CCTGCCATAAGCACCAACAAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTATAAGTTGT	806
Db	149	CCTGCCATAAGCACCAACAAGAACTTCTTGACAGGTGGAGTGGCTGTTTTTATAAGTTGT	90
Qy	807	TTTACAGATACGGAACAGTCCAAAATGGGATTATATAATTTCTTTTGCATTATAAATA	866
Db	89	TTTACAGATACGGAACAGTCCAAAATGGGATTATATAA-TTCTTTTGCATTATAAATA	31
Qy	867	AAGATCCTCTGTAAC	881
Db	30	AAGATCCTCTGTAAC	16

RESULT 12
BQ025360/c

LOCUS	BQ025360	581 bp	mRNA	linear	EST 27-MAR-2002
DEFINITION	UI-1-BB1p-aud-f-02-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone				
	UI-1-BB1p-aud-f-02-0-UI 3', mRNA sequence.				
ACCESSION	BQ025360				
VERSION	BQ025360.1 GI:19760639				

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 581)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source Location/Qualifiers

1..581

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-1-BB1p-aud-f-02-0-UI"

/tissue_type="Placenta"

/dev_stage="Full Term"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_P16"

/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_P16 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGAA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_TISSUE=placenta human full term
TAG_LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN

Qy	327	GAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	386
Db	569	GAGGACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGA	510
Qy	387	AGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	446
Db	509	AGCCTGAGGAGGTGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAG	450
Qy	447	GTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGC	506
Db	449	TTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACTGAGC	390
Qy	507	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	566
Db	389	GAACCCGGGCCTCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC	330
Qy	567	TTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	626
Db	329	TTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTT	270
Qy	627	CTTGCTGACTCCGGCCTGGTGAAGGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGG	686
Db	269	CTTGCTGACTCCGGCCTGGTGAAGGGGAGCGCCATGGTCTGGCTGTTGGGGTCCCAGGG	210
Qy	687	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	746
Db	209	AGAGGCTCTCTTCTGGACAAACACACCCTCCCAGCCCCCAGGGCTGTGCAAACACATGCC	150
Qy	747	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGT	806
Db	149	CCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGTGGCTGTTTTTTATAAGTTGT	90
Qy	807	TTTACAGATACGGAAACAGTCCAAAATGGGATTATATAATTCTTTTTTGCAATTATAAATA	866
Db	89	TTTACAGATACGGAAACAGTCCAAAATGGGATTATATAA-TTCTTTTTTGCAATTATAAATA	31
Qy	867	AAGATCCTCTGTAAAC	881
Db	30	AAGATCCTCTGTAAAC	16

LOCUS BM711587 591 bp mRNA linear EST 28-FEB-2002

DEFINITION UI-E-CL1-afb-g-19-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
 UI-E-CL1-afb-g-19-0-UI 5', mRNA sequence.

ACCESSION BM711587

VERSION BM711587.1 GI:19024845

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 591)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: Soares, MB
 Cancer Biology & Epigenomics Program
 Children's Memorial Research Center
 2300 Children's Plaza, Box 220, Chicago, IL 60614-3394, USA
 Tel: 773 755 6551
 Fax: 773 755 6378
 Email: mbsoares@childrensmemorial.org
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1..591
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-CL1-afb-g-19-0-UI"
 /tissue_type="human retina"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-CL1"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CL1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match	60.9%;	Score 536.4;	DB 4;	Length 591;
Best Local Similarity	96.0%;	Pred. No. 1.2e-120;		
Matches 549;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
Qy	307	ATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGAT	366	
Db	20	ATGGGGCTTAAGATGTCTCGCTGAAAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGAT	79	
Qy	367	GATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTG	426	
Db	80	GATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCTGGGTTTGGCTGGCTGGCTCCTG	139	
Qy	427	CTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAAT	486	
Db	140	CTCCAGCGGCCCGGCTTCAGGTGTCCGGGGCGTGGCTGCCTGGAGCAGGTGTGCTGAAT	199	
Qy	487	ACCCTGGATGGGAACTGAGCGAACC CGGGCTCCGCTCAGAGAGACGTGGCAGGACCAGC	546	
Db	200	ACCCTGGATGGGAACTGAGCGAACC CGGGCTCCGCTCAGAGAGACGTGGCAGGACCAGC	259	
Qy	547	GAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGG	606	
Db	260	GAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTCCTCCAGGCCCGCTGAGTGGACCGG	319	
Qy	607	ACCTCTGACACCTCCAGGTCTTGCTGACTCCGGCTGGTGAAGGGAGCGCCATGGTCC	666	
Db	320	ACCTCTGACACCTCCAGGTCTTGCTGACTCCGGCTGGTGAAGGGAGCGCCATGGTCC	379	
Qy	667	TGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGACAAACACACCTCCAGCCCCCA	726	
Db	380	TGGCTGTTGGGGTCNAGGGAGAGGCTCTCTTCTGGACAAACACACCTCCAGCCCCCA	439	
Qy	727	GGGCTGTGCAACACATGCCCTGCCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGT	786	
Db	440	GGGCTGTGCAACACATGCCCTCGCATAAGCACCAACAAGAACTTCTTGCAGGTGGAGT	499	
Qy	787	GGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAATGGGATTTATAATT	846	
Db	500	GGCTGTTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAATGGGATTTATAATT	559	
Qy	847	TCTTTTTTGCATTATAATAAAGATCCTCTGT	878	

Db 560 TCTTTTTTGCATTATAATANAGATCCTCTGT 591

RESULT 14
AI973037/c

LOCUS AI973037 539 bp mRNA linear EST 08-MAR-2000
DEFINITION wr46g08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2490782 3',
mRNA sequence.

ACCESSION AI973037

VERSION AI973037.1 GI:5769863

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 539)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 768 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 458.

FEATURES Location/Qualifiers

source 1. .539

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2490782"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA
from the normalized library NCI_CGAP_Pr22 was prepared,
and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match		60.8%; Score 536; DB 1; Length 539;					
Best Local Similarity		100.0%; Pred. No. 1.5e-120;					
Matches		536;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	345	TGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCT	404				
Db	539	TGAGACAGGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGGTGTCCT	480				
Qy	405	GGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCT	464				
Db	479	GGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGCGTGGCT	420				
Qy	465	GCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACCTGAGCGAACC CGGGCCTCCGCTC	524				
Db	419	GCCTGGAGCAGGTGTGCTGAATACCTGGATGGGAACCTGAGCGAACC CGGGCCTCCGCTC	360				
Qy	525	AGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCC	584				
Db	359	AGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACTTCCAGAACAGTGTTTCC	300				
Qy	585	CAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCCTTGCTGACTCCGGCCTG	644				
Db	299	CAGGCCCCGCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCCTTGCTGACTCCGGCCTG	240				
Qy	645	GTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGAC	704				
Db	239	GTGAAAGGGAGCGCCATGGTCCTGGCTGTTGGGGTCCCAGGGAGAGGCTCTCTTCTGGAC	180				
Qy	705	AAACACACCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAAC	764				
Db	179	AAACACACCTCCAGCCCCCAGGGCTGTGCAAACACATGCCCTGCCATAAGCACCAAC	120				
Qy	765	AAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTTATAAGTTGTTTACAGATACGGAAACA	824				
Db	119	AAGAACTTCTTGCAAGTGGAGTGGCTGTTTTTTATAAGTTGTTTACAGATACGGAAACA	60				
Qy	825	GTCCAAAATGGGATTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAA	880				
Db	59	GTCCAAAATGGGATTATAATTTCTTTTTTGCATTATAAATAAAGATCCTCTGTAA	4				

RESULT 15

CB993691
 LOCUS CB993691 843 bp mRNA linear EST 01-MAY-2003
 DEFINITION AGENCOURT_13624626 NIH_MGC_148 Homo sapiens cDNA clone
 IMAGE:30338285 5', mRNA sequence.

ACCESSION CB993691
 VERSION CB993691.1 GI:30288211
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM364 row: 1 column: 06
 High quality sequence stop: 408.

FEATURES
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 /mol_type="mRNA"
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 /clone="IMAGE:30338285"
 /tissue_type="pre-eclamptic placenta"
 /lab_host="DH10B TonA"
 /clone_lib="NIH_MGC_148"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamH; Library is oligo-dT primed and
 directionally cloned using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
 size 2.3 kb and normalized to ROT 5. This is a primary
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NIMH/NHGRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

ORIGIN

http://es.ScoreAccessWeb/GetItem.action?AppId=105295...7 122917 us-10-529-592a-1.rst&ItemType=4&startByte=0 (34 of 35)5/19/2009 9:51:32 AM

Search completed: April 28, 2009, 04:48:02

Job time : 1887 secs

SCORE 0.0